In the specification:

Please amend the specification as follows:

Please replace the first full paragraph that begins with "Tyrosine-based motifs ..." with the following paragraph:

--Tyrosine-based motifs are within the scope of the present invention as biological persistence and/or a biological activity altering components. Tyrosine-based motifs comprise the sequence Y-x-x-Hy (SEQ ID NO:23) where Y is tyrosine, x is any amino acid and Hy is a hydrophobic amino acid. Tyrosine-based motifs can act in a manner that is similar to that of leucine-based motifs. In figure 3 some of tyrosine motifs found in the type A toxin light chain are bracketed. In addition, a tyrosine-based motif is found within the leucine-based motif which is indicated by an asterisked bracket in figure 3.--

Please replace the paragraph bridging page 35 and 36 with the following paragraph:

--Figure 8 shows a sequence alignment between type A and type B light chains isolated from strains type A HallA (SEQ ID NO: 19) and type B Danish I (SEQ ID NO: 20) respectively. Light chains or heavy chains isolated from other strains of botulinum toxin types A and B can also be used for sequence comparison. The shaded amino acids represent amino acid identities, or matches, between the chains. Each of the shaded amino acids between amino acid position 10 and amino acid position 425 of the figure 8 consensus sequence, alone or in combination with any other shaded amino acid or amino acids, represents a biological persistence altering component that is within the scope of the present invention. For example, amino acids KAFK (SEQ ID NO: 21) at positions 19 to 22, LNK at positions 304 to 306, L at position 228 in combination with KL at positions 95 and 96, FDKLYK (SEQ ID NO: 22) at positions 346 to 351, YL-T at positions 78 to 81, YYD at positions 73 to 75 in combination with YL at positions 78 and 79 in combination with T a position 81, F at position 297 in combination with I at position 300 in combination with KL at positions 95 and 96 can be biological persistence altering

components for use within the scope of this invention. In addition, conserved regions of charge, hydrophobicity, hydro-philicity and/or conserved secondary, tertiary, or quaternary structures that may be independent of conserved sequence are within the scope of the present invention.--